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 | | |\/| |        | |   |   |  |    | |   |   |    | | | | | |
 | |\\/| | |\/|     | |__ | |   | |  | |   | |  | |   | | | | | |
 | | \/ | | |  |    | __| | |   | |  | |__ | |  | |   | |_| | | |
 | |    | | |  |    | |   | |   | |\\ | |  | |  | |    | | |  | |
 |_|    |_| |_|     |___| |_| \\_\\|__| |_|  |_|    |_| |_|  |_|  (TM)
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MPsrch_nn   n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Fri Aug 8 16:02:47 1997; MasPar time 1175.28 Seconds
                                          1326.024 Million cell updates/sec
Tabular output not generated.

Title: >N70819
Description: (1-1419) from us08476567.seq
Perfect Score: 1419
N.A. Sequence: 1 ccgagccgagaatgggagta..........aatagaggagtcaagttctt 1419
       Comp: ggctcggctcttaccctcat..........ttatctcctcagttcaagaa

Scoring table: TABLE default
                 Gap 6

Nmatch   STD : Dbase 0; Query 0

Searched: 362067 seqs, 549138275 bases x 2

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database: embl-new3
                 1:BCT 2:FUN 3:GEN1 4:GEN2 5:HTG1 6:HTG2 7:HUM 8:INV
                 9:ORG 10:MAM 11:VRT 12:PLN 13:PRO 14:ROD 15:SYN 16:UNC
                 17:VIR
Database: genbank99
                 18:BCT1 19:BCT2 20:BCT3 21:BCT4 22:BCT5 23:BCT6 24:BCT7
                 25:BCT8 26:BCT9 27:BCT10 28:BCT11 29:GEN1 30:GEN2
                 31:GEN3 32:HTG1 33:HTG2 34:HTG3 35:INV1 36:INV2 37:INV3
                 38:INV4 39:INV5 40:INV6 41:INV7 42:INV8 43:INV9 44:INV10
                 45:INV11 46:MAM1 47:MAM2 48:MAM3 49:VRT1 50:VRT2 51:VRT3
                 52:VRT4 53:PAT1 54:PAT2 55:PAT3 56:PAT4 57:PAT5 58:PHG
                 59:PLN1 60:PLN2 61:PLN3 62:PLN4 63:PLN5 64:PLN6 65:PLN7
                 66:PLN8 67:PLN9 68:PLN10 69:PLN11 70:PRI1 71:PRI2
                 72:PRI3 73:PRI4 74:PRI5 75:PRI6 76:PRI7 77:PRI8 78:PRI9
                 79:PRI10 80:PRI11 81:PRI12 82:PRI13 83:PRI14 84:PRI15
                 85:ROD1 86:ROD2 87:ROD3 88:ROD4 89:ROD5 90:ROD6 91:ROD7
                 92:ROD8 93:STR 94:SYN 95:UNA 96:VRL1 97:VRL2 98:VRL3
                 99:VRL4 100:VRL5 101:VRL6 102:VRL7 103:VRL8 104:VRL9
                 105:VRL10
Database: genbank-new3
                 106:BCT 107:GEN1 108:GEN2 109:HTG1 110:HTG2 111:INV
                 112:MAM 113:VRT 114:PHG 115:PLN 116:PRI1 117:PRI2
                 118:ROD 119:SYN 120:UNA 121:VRL
Database: u-embl50_99
                 122:part1

Statistics: Mean 11.369; Variance 4.112; scale 2.765

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

                              SUMMARIES
                        %
Result   Query
  No. Score Match Length DB ID   Description   Pred. No.
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```
--------------------------------------------------------------------------------
    1   1419  100.0    1419 53  A12480      cDNA for glutamine sy  0.00e+00
    2   1419  100.0    1421 85  CLGSR       Chinese hamster mRNA   0.00e+00
    3   1003   70.7    2731 85  MMGSASE     M.musculus mRNA for g  0.00e+00
    4    943   66.5    1150 86  MMU09114    Mus musculus glutamat  0.00e+00
    5    926   65.3    2787 92  RRGS        Rat mRNA for glutamin  0.00e+00
    6    926   65.3    2787 90  RATGLUS     R.norvegicus glutamin  0.00e+00
    7    921   64.9    1366 74  HSGLUSYN    Human mRNA for glutam  0.00e+00
    8    919   64.8    2727 74  HSGLUS      Human rearranged mRNA  0.00e+00
    9    917   64.6    2793 90  RATGLNAB    Rat glutamine synthet  0.00e+00
   10    911   64.2    2631 84  S70290      glutamine synthetase   0.00e+00
   11    898   63.3    1370 48  SSGLUSYN    S.scrofa mRNA for glu  0.00e+00
   12    881   62.1    2925 88  MUSGSA      Mouse intronless glut  0.00e+00
   13    812   57.2    3004 77  HSU08626    Human glutamine synth  0.00e+00
   14    673   47.4    1838 51  S45408      glutamine synthetase   0.00e+00
   15    671   47.3    2728 49  CHKGLN      Chicken retinal gluta  0.00e+00
   16    572   40.3    2753 51  SAU04617    Squalus acanthias glu  0.00e+00
   17    450   31.7    1617 52  XELXGS      Xenopus laevis mRNA f  0.00e+00
   18    449   31.6    1851 88  MUSGLN1     Mouse glutamine synth  0.00e+00
   19    342   24.1    2935 43  PALGLUSYN   Paracentrotus lividus  0.00e+00
   20    299   21.1    2045 44  PNLGTSYN    Panulirus argus gluta  3.85e-298
   21    251   17.7     386 46  BOVGLN      Bovine glutamine synt  8.10e-243
   22    247   17.4    2371 90  RATGLUSG6   Rat glutamine synthet  3.15e-238
   23    218   15.4    1496 39  DMGS2       D.melanogaster GS2 mR  4.68e-205
   24    192   13.5    2162 39  DMGS1       D.melanogaster GS1 mR  1.63e-175
   25    181   12.8     649 90  RATGLUSG5   Rat glutamine synthet  4.39e-163
   26    172   12.1    2424 60  COGGLN      Colletotrichum gloeos  5.97e-153
   27    145   10.2    1354 60  BNGLN       B.napus mRNA for glut  8.77e-123
   28    145   10.2    1780 69  YSCGLN1     S.cerevisiae glutamin  8.77e-123
   29    145   10.2   10339 65  SC3085      S.cerevisiae chromoso  8.77e-123
   30    145   10.2  165536 65  SCCHRXVI    S.cerevisiae chromoso  8.77e-123
   31    143   10.1    1450 65  S46513      cytosolic glutamine s  1.45e-120
   32    142   10.0     387 90  RATGLUSG2   Rat glutamine synthet  1.86e-119
   33    136    9.6    1326 64  RADGS1GC    Raphanus sativus mRNA  8.02e-113
   34    136    9.6    1429 63  LSGLUSYN    L.sativa mRNA for glu  8.02e-113
   35    135    9.5    1440 62  LJCYTGLSY   L.japonica mRNA for c  1.02e-111
   36    134    9.4    1317 69  ZMGS13      Z.mays mRNA gsl-3 for  1.29e-110
   37    134    9.4    1490 69  ZMGS14      Z.mays mRNA gsl-4 for  1.29e-110
   38    132    9.3    1332 64  PSGSISO     P.sylvestris mRNA for  2.06e-108
   39    132    9.3    1350 63  MZEGS1B     Maize mRNA for glutam  2.06e-108
   40    132    9.3    1422 63  MZEGS1A     Maize mRNA for glutam  2.06e-108
   41    131    9.2    1484 64  RADGS1BB    Raphanus sativus mRNA  2.60e-107
   42    130    9.2    1553 63  OSSIGS28    Oryza sativa shoot GS  3.27e-106
   43    131    9.2    1649 63  OSSIGS31    Oryza sativa shoot GS  2.60e-107
   44    129    9.1    1454 64  PVGSR1      Phaseolus vulgaris mR  4.10e-105
   45    129    9.1    1483 69  ZMGS2       Z.mays mRNA gs2 for g  4.10e-105
```

ALIGNMENTS

```
RESULT     1
LOCUS       A12480         1419 bp    RNA              PAT       09-DEC-1993
DEFINITION  cDNA for glutamine synthatase.
ACCESSION   A12480
NID         g490275
KEYWORDS    .
SOURCE      long-tailed hamster.
  ORGANISM  Cricetulus longicaudatus
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
            Cricetinae; Cricetulus.
REFERENCE   1  (bases 1 to 1419)
  AUTHORS   .
  TITLE     RECOMBINANT DNA SEQUENCES, VECTORS CONTAINING THEM AND METHOD FOR
            THE USE THEREOF
  JOURNAL   Patent: WO 8704462-A 1 30-JUL-1987;

FEATURES             Location/Qualifiers
     source          1..1419
                     /organism="Cricetulus longicaudatus"
     CDS             145..1266
                     /gene="GS gene"
                     /codon_start=1
                     /db_xref="PID:g490276"
                     /db_xref="SWISS-PROT:P04773"
```

```
Db    270 ggaactttgatggctccagcaccttccaagccgaaggctccaacagcgacatgtacctgc 329
          |||| ||||||||||| || ||||| || | || |||||||||||| |||||||| ||
Qy    323 ggaattttgatggctctagtacctttcagtctgagggctccaacagtgacatgtatctca 382

Db    330 gacctgctgccatgttccgggacccttttcgcaaggatcccaacaaattagttctctgtg 389
          | |||| ||||||||||| ||||||||| || |||| ||||||||||||| | || ||||||
Qy    383 gccctgttgccatgtttcgggaccccttccgcagagatcccaacaagctggtgttctgtg 442

Db    390 aggtcttcaaatacaaccgccagtctgcagacacaaatcttcggcacacctgtaggcgga 449
          | || |||| |||||||| || |||||||| || ||| | |||||| | ||||| ||||
Qy    443 aagttttcaagtacaaccggaagcctgcagagaccaatttaaggcactcgtgtaaacgga 502

Db    450 ttatggatatggtgtccaaccagcacccctggtttgggatggagcaggagtacacccttc 509
          | ||||| |||||| |||||||||||||||||||| ||||| ||||| ||||||||| || ||
Qy    503 taatggacatggtgagcaaccagcacccctggtttggaatggaacaggagtatactctga 562

Db    510 tgggaacagatggtcatccgtttggctggccttccaattgcttccctggaccccaaggtc 569
          |||||||||||||| || || ||||| |||||||||||||| |||| |||||| ||||||||||
Qy    563 tgggaacagatgggcacccttttggttggccttccaatggctttcctgggccccaaggtc 622

Db    570 cgtactactgcggtgtaggagctgacaaagcctatggcagagacattgtggaggcccact 629
          |||| ||||| ||||| || || |||||||||||||||||| || || ||||||||| ||||
Qy    623 cgtattactgtggtgtgtgggcgcagacaaagcctatggcagggatatcgtggaggctcact 682

Db    630 accgagcgtgcctgtatgctggtgtgaaaattggaggaaccaacgcagaagtgatgccag 689
          |||| || ||| |||||||||||| || || ||| |||||| || || || |||||| |
Qy    683 accgcgcctgcttgtatgctggggtcaagattacaggaacaaatgctgaggtcatgcctg 742

Db    690 cccagtgggagttccaggtgggaccgtgcgaagggattgagatgggggatcacctctgga 749
          ||||||||| ||||| | ||||| || ||||| || ||||| ||||| |||||
Qy    743 cccagtgggaattccaaataggaccctgtgaaggaatccgcatgggagatcatctctggg 802

Db    750 tagcacgtttcatcctccaccgggtgtgcgaagactttggtgtcattgtgtccttcgatc 809
          | || ||||||||||| | || || || || || |||||||||| || || | |||| || |
Qy    803 tggcccgtttcatcttgcatcgagtatgtgaagactttggggtaatagcaaccttttgacc 862

Db    810 ccaaacccatccctgggaactggaacggtgctggctgtcacaccaacttcagcaccaaga 869
          |||| |||||| |||||||||||||||| ||||| ||||| || || |||||||| |||||||||
Qy    863 ccaagcccattcctgggaactggaatggtgcaggctgccataccaactttagcaccaagg 922

Db    870 acatgagggaagatggaggtctcaagcacatcgaggaggccatcgagaagctgagcaagc 929
           |||| |||| || ||||| || |||||||||||||||||||| || |||||||
Qy    923 ccatgcgggaggagaatggtctgaagcacatcgaggaggccatcgagaaactaagcaagc 982

Db    930 gccaccagtaccacatccgtgcctacgaccccaaaggagggctggacaacgcccggcgcc 989
          | |||| |||||||| || ||||||||| ||||| || || ||||||||| ||||| | |
Qy    983 ggcaccggtaccacattcgagcctacgatcccaaggggggcctggacaatgcccgtggtc 1042

Db    990 tgacgggcttccacgagacgtccagcatccacgagttctccgccggcgtggccaaccgcg 1049
          |||| || ||||||||| ||||||| |||| |||| || || || || || ||||| |||
Qy   1043 tgactgggttccacgaaacgtccaacatcaacgacttttctgctggtgtcgccaatcgca 1102

Db   1050 gcgccagcatccgcatcccacgcaacgtgggccatgagaagaaaggctacttcgaggacc 1109
          | |||||||||||||| || || | || ||||| ||||||||||| ||||| | |||||
Qy   1103 gtgccagcatccgcattccccggactgtcggccaggagaagaaaggttactttgaagacc 1162

Db   1110 gcgggccttcagccaactgcgatccctacgccgtgacggaggccctggtccgtacgtgtc 1169
          || | || || ||||| || || |||| || ||||| || ||| | ||||| || || |
Qy   1163 gccgccctctgccaattgtgaccccctttgcagtgacagaagccatcgtccgcacatgcc 1222

Db   1170 tcctcaacgaaaccggggacgagccttttgagtacaagaactaagtggact 1220
          | ||||| || || || ||||||||| || | ||||| |||||| | ||||
Qy   1223 ttctcaatgagactggcgacgagcccttccaatacaaaaactaattagact 1273


Search completed: Fri Aug  8 16:45:36 1997
Job time : 2569 secs.

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 | |         | |  | |              | |  | |\\   | |        | |     | |
 | |         | |  | |           __| |  | |\\   | |__      | |     | |
 |_|         |_| |_|          |____|  |_|  \_\ |____|    |_|     |_|    (TM)
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MPsrch_nn   n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Fri Aug 8 16:45:55 1997; MasPar time 133.41 Seconds
                                             984.006 Million cell updates/sec
Tabular output not generated.

Title: >N70819
Description: (1-1419) from us08476567.seq
Perfect Score: 1419
N.A. Sequence: 1 ccgagccgagaatgggagta..........aatagaggagtcaagttctt 1419
      Comp: ggctcggctcttaccctcat..........ttatctcctcagttcaagaa

Scoring table: TABLE default
                  Gap 6

Nmatch   STD :   Dbase 0; Query 0

Searched: 121476 seqs, 46255616 bases x 2

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database: n-geneseq26
                 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
                 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
                 14:part14 15:part15 16:part16 17:part17 18:part18
                 19:part19 20:part20 21:part21 22:part22 23:part23

Statistics: Mean 9.364; Variance 4.957; scale 1.889

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
```

	Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
	1	1419	100.0	1419	2	N70819	Sequence encoding chi	0.00e+00
	2	1187	83.7	13254	23	T40915	Nucleotide sequence o	0.00e+00
	3	134	9.4	1429	1	N91849	Lettuce glutamine syn	2.62e-79
	4	130	9.2	1255	1	Q05727	Gene encoding glutami	3.03e-76
	5	131	9.2	1649	2	Q10333	Encodes Rice chloropl	5.20e-77
	6	128	9.0	1200	1	Q05728	Gene encoding glutami	1.02e-74
	7	127	8.9	1262	1	Q05729	Gene encoding glutami	5.95e-74
	8	124	8.7	1338	2	N70758	Sequence encoding alf	1.16e-71
	9	122	8.6	1068	2	N71176	Sequence encoding mut	3.86e-70
	10	79	5.6	246	22	T26426	Human gene signature	5.44e-38
	11	76	5.4	1047	2	Q10572	Human Natriuretic Pep	8.29e-36
c	12	77	5.4	1047	2	Q10572	Human Natriuretic Pep	1.56e-36
	13	58	4.1	185	2	N70762	Partial sequence of t	5.56e-23
	14	58	4.1	221	2	N70760	Partial sequence of t	5.56e-23
	15	47	3.3	1200	1	N90907	Glutamine synthesis g	1.84e-15
	16	45	3.2	91	9	Q51746	Oligonucleotide probe	3.93e-14
	17	46	3.2	4464	2	N71244	Genomic sequence of a	8.53e-15
	18	46	3.2	4465	5	Q28697	Glutamine synthetase.	8.53e-15
c	19	43	3.0	91	9	Q51746	Oligonucleotide probe	8.14e-13
c	20	42	3.0	204	1	N81164	Base substituted E.co	3.66e-12
	21	43	3.0	312	2	N70764	Partial sequence of t	8.14e-13
	22	41	2.9	204	1	N81164	Base substituted E.co	1.63e-11
	23	37	2.6	348	6	Q39897	Expressed Sequence Ta	5.78e-09
	24	37	2.6	348	8	Q59309	Human brain Expressed	5.78e-09
	25	36	2.5	114	12	Q70467	Generic DNA sequence	2.44e-08
	26	34	2.4	48	18	T13986	Glutamine synthetase	4.19e-07

	27	34	2.4	114	12	Q70468	Generic DNA sequence	4.19e-07
	28	34	2.4	114	12	Q70465	Generic DNA sequence	4.19e-07
	29	33	2.3	114	12	Q70470	Generic DNA sequence	1.70e-06
	30	32	2.3	114	12	Q70472	Generic DNA sequence	6.80e-06
	31	32	2.3	114	12	Q70469	Generic DNA sequence	6.80e-06
c	32	32	2.3	114	12	Q70469	Generic DNA sequence	6.80e-06
c	33	32	2.3	114	12	Q70468	Generic DNA sequence	6.80e-06
	34	33	2.3	200	2	N70759	Partial sequence of t	1.70e-06
	35	31	2.2	114	12	Q70471	Generic DNA sequence	2.68e-05
c	36	31	2.2	114	12	Q70467	Generic DNA sequence	2.68e-05
	37	30	2.1	114	12	Q70466	Generic DNA sequence	1.04e-04
c	38	30	2.1	114	12	Q70470	Generic DNA sequence	1.04e-04
c	39	30	2.1	114	12	Q70465	Generic DNA sequence	1.04e-04
c	40	30	2.1	501	3	N50023	Sequence encoding new	1.04e-04
	41	29	2.0	114	12	Q70473	Generic DNA sequence	3.95e-04
c	42	29	2.0	114	12	Q70466	Generic DNA sequence	3.95e-04
c	43	28	2.0	501	3	N50026	Sequence encoding new	1.48e-03
c	44	28	2.0	501	3	N50033	Sequence encoding new	1.48e-03
c	45	26	1.8	114	12	Q70471	Generic DNA sequence	1.94e-02

ALIGNMENTS

```
RESULT      1
ID     N70819 standard; cDNA; 1419 BP.
AC     N70819;
DT     13-MAY-1991   (first entry)
DE     Sequence encoding chinese hamster glutamine synthetase.
KW     DHFR/MTX; ss.
OS     Cricetulus griseus.
FH     Key             Location/Qualifiers
FT     stem_loop       7..80
FT     /*tag=   a
FT     stem_loop       81..130
FT     /*tag=   b
FT     CDS             145..1266
FT     /*tag=   c
PN     WO8704462-A.
PD     30-JUL-1987.
PF     23-JAN-1987; GO0039.
PR     23-JAN-1986; GB-001597.
PA     (CELL-) CELLTECH LTD.
PA     (UNIU ) UNIV OF GLASGOW.
PA     (WILS/) WILSON RH.
PI     Wilson RH, Bebbington CR;
DR     WPI; 87-221263/31.
DR     P-PSDB; P70501.
PT     Recombinant DNA which encodes glutamine synthetase - used esp. in
PT     co-amplification of non-selected genes and in transforming host
PT     cell lines.
PS     Claim 6; Fig 2a-e; 54pp; English.
CC     Sequence may be used as a hybridisation probe in the isolation of the
CC     GS gene in other species, and as a diagnostic tool in the detection
CC     of diseases altering GS expression. A second use is as a selectable
CC     marker in recombinant DNA technology eg. co-amplification selection,
CC     or transformation to glutamine independence.
SQ     Sequence   1419 BP;     338 A;     391 C;     361 G;     329 T;

  Query Match              100.0%;   Score 1419;  DB 2;  Length 1419;
  Best Local Similarity 100.0%;   Pred. No. 0.00e+00;
  Matches  1419;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;


Db      1 ccgagccgagaatgggagtagagccgactgcttgattcccacaccaatctcctcgccgct 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      1 ccgagccgagaatgggagtagagccgactgcttgattcccacaccaatctcctcgccgct 60


Db     61 ctcacttcgcctcgttctcgtggctcgtggccctgtccaccccgtccatcatcccgccgg 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     61 ctcacttcgcctcgttctcgtggctcgtggccctgtccaccccgtccatcatcccgccgg 120


Db    121 ccaccgctcagagcaccttccaccatggccacctcagcaagttcccacttgaacaaaaac 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    121 ccaccgctcagagcaccttccaccatggccacctcagcaagttcccacttgaacaaaaac 180


Db    181 atcaagcaaatgtacttgtgcctgccccagggtgagaaagtccaagccatgtatatctgg 240
```